SEQUENCE LISTING

<110> Hart, Charles E.
      Topouzis, Stavros

<120> COMPOSITIONS AND METHODS FOR IMPROVING
      KIDNEY FUNCTION

<130> 00-100

<150> US 60/244,479
<151> 2000-10-30

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (226)...(1338)

<400> 1
ccgtcaccat ttatcagctc agcaccacaa ggaagtgcgg cacccacacg cgctcggaaa      60
gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg     120
cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac     180
ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc     237
                                                   Met His Arg Leu
                                                    1

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac     285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
 5               10               15               20

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc     333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
             25               30               35

```
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga          381
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
            40              45                  50

gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga          429
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
        55              60                  65

ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac          477
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
    70              75                  80

tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga          525
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
85                  90                  95                  100

tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt          573
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val
                105                 110                 115

gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga          621
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly
            120                 125                 130

cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa          669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys
        135                 140                 145

atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag          717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys
        150                 155                 160

att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag          765
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu
165                 170                 175                 180

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac          813
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn
                185                 190                 195

tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa          861
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys
            200                 205                 210
```

```
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat     909
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn
        215             220             225

cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct     957
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro
    230             235             240

cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg     1005
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu
245             250             255             260

gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat     1053
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn
                265             270             275

tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc     1101
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe
            280             285             290

ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt     1149
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys
        295             300             305

gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg     1197
Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val
        310             315             320

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg     1245
Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
325             330             335             340

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac     1293
Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
                345             350             355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa        1338
His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg  *
                360             365             370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtgagat  1398
```

```
aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca    1458
agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca    1518
tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga ggttatatat    1578
gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt    1638
ttttggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa    1698
tcctttgcca aaataaggga tggtcaaata tatgaaacat gtctttagaa aatttaggag    1758
ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa    1818
agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat    1878
tatt                                                                 1882
```

<210> 2
<211> 370
<212> PRT
<213> Homo sapiens

<400> 2

```
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
1               5                   10                  15
Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
            20                  25                  30
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
        35                  40                  45
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
    50                  55                  60
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65                  70                  75                  80
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
                85                  90                  95
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
                100                 105                 110
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
            115                 120                 125
Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
    130                 135                 140
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145                 150                 155                 160
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
                165                 170                 175
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
            180                 185                 190
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
        195                 200                 205
```

```
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
    210             215             220
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225             230             235             240
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
            245             250             255
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
            260             265             270
Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
            275             280             285
Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
    290             295             300
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305             310             315             320
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
            325             330             335
His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
            340             345             350
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
    355             360             365
Pro Arg
    370
```

```
<210> 3
<211> 1472
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (93)...(1205)

<400> 3
```

```
agggactgtg cagtagaaat ccgccgactc aaccctttgg gctttatttta tttactttg      60
gagcaacgcg atccctaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc     113
                                   Met Gln Arg Leu Val Leu Val
                                    1               5

tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg     161
Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
        10              15              20
```

```
act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg    209
Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
     25              30                  35


aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac    257
Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
 40              45                  50                  55


att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac    305
Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
                 60                  65                  70


agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag    353
Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu
                 75                  80                  85


aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa    401
Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu
                 90                  95                  100


gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc    449
Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu Val
                 105                 110                 115


tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag    497
Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu
120                 125                 130                 135


atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt    545
Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe
                 140                 145                 150


aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat    593
Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr
                 155                 160                 165


tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg    641
Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp
                 170                 175                 180


gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca    689
Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser
                 185                 190                 195
```

```
ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca      737
Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala
200             205             210             215

gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct      785
Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser
            220             225             230

tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga      833
Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg
            235             240             245

ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc      881
Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu
            250             255             260

aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg      929
Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val
            265             270             275

aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga      977
Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg
280             285             290             295

tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc      1025
Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val
            300             305             310

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat      1073
Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr
            315             320             325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa      1121
His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys
            330             335             340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga      1169
Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg
            345             350             355
```

```
tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc          1215
Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg  *
360                 365                 370


acatctgtac tttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa  1275
tctcagtgca atgaatgcat atggaaatgt tgctttgtta gtgccatggc aagaagaagc  1335
aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtatgtgaag  1395
atatgtatat atacttatat acatgactag ctctatgtat gtaaatagat taaatacttt  1455
attcagtata tttactg                                                 1472
```

```
<210> 4
<211> 370
<212> PRT
<213> Mus musculus


<400> 4
Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser
1               5               10              15
Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
            20              25              30
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
        35              40              45
Leu Tyr Gln Arg Glu Glu Asn Ile Gln Val Thr Ser Asn Gly His Val
    50              55              60
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65              70              75              80
Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp
            85              90                  95
His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
            100             105             110
Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly
        115             120             125
Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr
    130             135             140
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145             150             155             160
Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu
            165             170             175
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly
        180             185             190
Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp
    195             200             205
```

```
Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
    210             215             220
Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr
225                 230             235                 240
Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
                245             250                 255
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys
            260             265             270
Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr
            275             280             285
Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
    290             295             300
Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
305                 310             315                 320
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
                325             330                 335
His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
            340             345             350
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
    355             360             365
Pro Arg
    370


    <210> 5
    <211> 24
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> oligonucleotide primer ZC21,987

    <400> 5
caacctgttg tttgtcccgt cacc


    <210> 6
    <211> 24
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> oligonucleotide primer ZC21,120

    <400> 6
```

24

tccagagcat ccgcaatcag agtg 24

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC26317

<400> 7
atcacctcac agacttgtac cagag 25

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC26318

<400> 8
cctacaaatg tcattttctg cttcc 25

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 9
Glu Tyr Met Pro Met Glu
1               5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 10
Glu Tyr Met Pro Thr Asp
1              5